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AAY76144
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12-MAY-1998;
                                                                                                                                                                                                                                                                                                           Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; dispetive disorder; endocrine disorder; infection; AIDS; leukaemia;
                                                         06-MAY-1999;
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                                                                                                                                                                                 WO9958660-A1
                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein encoded by gene 21.
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                                                                                                                                                                                                                                                                                                                                                                 AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes. CC AAY76124 to AAY76223 are the secreted proteins encoded by the 97 human cc genes. The gene encoding this protein was found to be on chromosome 18q22 for preventing, treating or ameliorating medical conditions are useful protein or gene therapy. Also pathological conditions can be diagnosed by cetermining the amount of the new polypeptides in a sample or by cdetermining the presence of mutations in the new genes. Specific uses are described for each of the 97 genes, based on which tissues they are most treatment of cancer, tumours, developmental abnormalities and foetal cdiseases, inflammation, allergies, Alzheimer's and cognitive disorders, catherosclerosis, diabetes, cardiovascular disorders, kidney disorders, calso useful for identifying their binding partners. The sequences shown or analytical and analytical and analytical and analytical are recommended to the secreted proteins shown or analytical to AAY76224 to AAY76424 represent fragments of the secreted proteins
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 507; Conserv
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Olsen
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12-MAY-1998;
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N-PSDB; AAZ65270.
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Search completed: February 17, 2005, 15:19:48 Job time : 0.001 secs	Search comp Job time :
481 QNEKINRWIYIEGTKLFAAFFLEWAQLH 508	Db .
480 QNEKINRWNYIEGTKLFAAFFLEMAQLH 507	Qy 4
421 ANIDDTQYLAAKRAIRTVFGTEEDMIRDGSTIFIAKMFQEIVHKSVVLIFLGAVDDGEHS 480	Db . 4
420 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 479	92
361 GTKTVIPGRVIGKFSIRLVPHMNVSÅVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420	Db 3
360 GTKTVIPGRVIGKFSIRLVPHYNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 419	Qy 3
301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360	pb 3
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Maximum Match 100%
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      12-MAY-1998;
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                                                                  06-MAY-1999;
                                                                                                                                  18-NOV-1999.
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2005 Compu
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Olsen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
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Search completed: February 17, 2005, 15:19:48 Job time : 0.001 secs

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                 11-DEC-1997;
                                              11-DEC-1998;
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                                                                                                                                       Listeria monocytogenes.
                                                                                                                                                                    Fanconi's anaemia; group C complementation

    monocytogenes dapE protein.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC expression, causing transcription and expression of foreign DNA and/or CC foreign protein in the location. The method is used for induced somatic CC gene therapy, immunological protection against microbes or protection against tumours. Listeria monocytogenes can be modified so that it has CC against tumours. Listeria monocytogenes can be modified so that it has CC are then secreted into, e.g. milk. Examples of where the method are useful, include treatment of cystic fibrosis (by manipulation of an CC airborne bacteria), treatment of beta-thalassemia by ex vivo modification CC of a haematopoietic cell to contain beta-globulin, for treatment of CC transformation/modification of CD34+ cells of the bone marrow with an CC complementation gene and also to treat Fanconi's anaemia with a group C complementation gene. The method does not require genetic CC transformation/modification of the organism requiring gene therapy. The CC expression of a therapeutic foreign protein by a bacteria that infects an animal is advantageous in that the expression can be tissue- or organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conditioning (TGC) for inducing targeted somatic transgenesis in an animal host where a bacteria comprising a foreign DNA integrated into an episomal vector releases, in the case of infection of a foreign organism, organ, tissue, cell line or individual cells, the foreign DNA under the control of eukaryotic regulatory elements for later transcription and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel bacterium modified to release a foreign DNA under the control of eukaryotic regulatory elements into a foreign organism, organ, tissue, cell line or individual cells after infection of the host. The method of the invention allows a targeted genetic conditioning (TGC) for inducing targeted somatic transgenesis in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (VBIC/)
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237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 VCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 6.7%; Score 176; DB 1; L
Similarity 22.4%; Pred. No. 0;
83; Conservative 55; Mismatches 158;
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                                                                                                                                                                                                              EBBINTYKAIHLDLEBYRNSSRVEKFL--FDTKBBILMHLWRYPSLSIHGIBGAFDEPGT 361
                                                                                                                                                                                                                                                           KGSINY -- PVKSTGKNAHSS
                                                                                                                                                                                                                                                                                                                                             LNGKIRLLATVGEEIGELGAEQLTQK---GYADDLHGLIIGE--
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                                                                                 VNSIPEKAQLQGNIRSIPEMDNETV-KQVLVKIINKLNKQSNVNLELI-FDYDKQPVFSD
                                                                                                                          KTVIPGRVIGKFSIRLVPHMNVSAVEKOVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIAN
                                                                                                                                                                     ESGVNAIDNLLLFYNE----VEKFVKSVDATNBILGDF---
  KNSDLVHIAKSVASDIVKEEIPLLGISGTTDAABFTK--AKKEFPVIIFGPGNETPHQVN
                                        IDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQBIVHKSVVLIPLGAVDDGEHSQN
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Search completed: February 17, 2005, 15:23:27 Job time : 1 secs

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RESULT 1
AAW19339
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                                                                                                                                                                                                                                 17-OCT-2003
25-MAR-2003
11-MAR-1998
                                                                                                                Human immunodeficiency virus 1. Escherichia coli.
 28-FEB-1992;
                        28-FEB-1992;
                                                   10-JAN-1997.
                                                                           RU2071502-C1
                                                                                                                                                                  Hybrid; chimeric; fusion; polypeptide; P102; detection; antibody; VCPM B-5876; pol; beta-galactosidase; reverse transcriptase;
                                                                                                                                                                                                      Hybrid polypeptide P102 for detecting antibodies to HIV-1.
                                                                                                                                                                                                                                                                                      AAW19339;
                                                                                                                                                                                                                                                                                                            AAW19339 standard; protein;
                                                                                                                                                       immunodetection; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                    57
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length: 2000000000
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125.229 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                  Sequence 247 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Col 11; 6pp; Russian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hybrid polypeptide P102 for detecting antibodies to HIV-1 - comprises HIV-1 reverse transcriptase fused to E.coli beta-galactosidase.
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N-PSDB; AAT73713.
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                                                                 220
                                                                                                                                    164
                                                                                                                                                                                                    114 DIQKLVGKLNMASQ--IYPGIKVRQLCKLLRGTKALTEVVPLTEEA------LELAEN 163
                                                                                                                                                                                                                         275 DLVALLGSIVDSSGHILVPGI------YDEVVPLTEEBINTYKAIHLDLEEY 320
                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                   REILKEPVHGVYYDPSKDLIAEIQKQG----QGPEAALQDSGLEVNIITDSQYALGIQAQ 219
                                                                                                                                                                    RN--SSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLV 378
                                                                 PDKSESELVNQIIEQL
                                                                                                  PHMNVSAVEKQVTRHL 394
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Pred. No. 0;
                                                                                                                                                                                                                                                                      Mismatches
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             Fischbach GD;
                                                                29-MAY-1991;
                                                                                        29-MAY-1991;
                                                                                                                  17-AUG-1993.
                                                                                                                                           US5237056-A.
                                                                                                                                                                     Gallus.
                                                                                                                                                                                             acetylcholine receptor-inducing activity protein; ARIA; E18
                                                                                                                                                                                                                      Sequence encoded by chicken brain cDNA encoding aceylcholine receptor-inducing activity (ARIA) protein E18.
                                                                                                                                                                                                                                                             08-FEB-1994
                                                                                                                                                                                                                                                                                       AAR40171;
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                                      (HARD ) HARVARD COLLEGE
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135.369 Million cell updates/sec
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                                                                                                                                                                                                                                                                                          ARIA promotes the synthesis and accumulation of acetylcholine receptors (AChRs) in muscle cells. The protein was isolated on the basis of its ability to increase the rate of insertion of AChRs into the surface membrane of chick myotubes. Oligos with sequences corresp. to the sequence of the protein were used to amplify from chicken brain cDNA a 34 nucleotide sequence encoding 11 AAs from ARIA. The 34 nucleotide sequence corresp. to the 3′ nucleotides of the 7th AA codon through the 1 nucleotide of the 18th AA codon. Each primer contd. an EcoRI site at 1 its 5′ end. The first pair of oligos are AAQ46887/Q46883. The second pair are AAQ46884/Q46885. The oligos are AAQ46887/Q46883. The second primer contains a probe to screen an E18 chick brain cDNA library. AAQ46887 is the insert from a positive clone obtd. by the screening an E18 chick brain cDNA library in lambda gt10 and introduced into a plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding protein which co-purifies with acetyl:choline receptor-inducing activity - used to obtain prods. for treating deficiencies in neural transmitter receptors, e.g. Alzheimer's disease.
                                                                                                                                                                                                                                        Sequence 267 AA;
                                                                                                                                                                                                                                                                              designated p65-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 2; 17pp; English.
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N-PSDB; AAQ46887.
                                                                                                                                                         Local Similarity es 9; Conserv
                                                                              249
                                                                                                     9 AASLLAVLLLLL 20
                                                                              ADTWLAVLLLLL
                                                                                                                                                             Conservative
                                                                                                                                                                              1.3%;
75.0%;
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing:
                                                                                                                                                                                         Human mGluR1B
                                                                                                                                                                                                                                                                       AAR64250 standard; protein;
          Daggett
                                                      04-JUN-1993;
                                                                            03-JUN-1994;
                                                                                                  22-DEC-1994.
                                                                                                                       WO9429449-A1
                                                                                                                                              Homo sapiens
                                                                                                                                                                   Metabotropic glutamate receptor; mGluR1; mGluR1B; cerebellum; pCMV-T7-3.
                                                                                                                                                                                                               25-MAR-2003
21-JUL-1995
                                                                                                                                                                                                                                                 AAR64250;
                                (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
          Ellis SB,
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                                                                                                                                                                                                               (revised)
(first entry)
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                                                                             94WO-US006273
                                                       93US-00072574.
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          Liaw C,
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          Pontsler A,
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          Johnson
          EC,
                                                                                                                                                                                                                                                                                                                                                               Human mGluR1B.
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           Hess
           SD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA encoding human metabotropic glutamate receptor sub:type(s) - an related proteins, probes, RNA, transformed cells and antibodies, useful in treatment, diagnosis and identification of specific modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mGluR1 receptor. Several clones were isolated, and a complete sequence was obtained by ligating overlapping clones. The resulting construct (given in AAQ80416) encoded human mGluR1B (AAR64250). The encoding sequence was operatively linked to the regulatory elements in pCMV-T7-3 for expression in mammalian cells. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-036478/05.
N-PSDB; AAQ80416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 906 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A human cerebellum cDNA library was screened with DNA encoding the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 75-79; 125pp; English.
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                                                                          463
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                                                                                                                                                                                                                                                                                                                                                                                                                 173 WINAVSA-----FRALEQDLP-----VNIKFIIEGMEEAGSVALEELVE 211
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                                                                                                                                                                                                                                                                                                                                     212 K----EKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFM---VEVKCRD---QDFH 261
                                                                                                                                                                                                                          QHRFQCRLPGHLLENPNFKRICTGNESLEENYVQDSKMGFVINAIYAMAHGLQNMHHALC 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -FLRVVPSDTLQARAMLDIVKRYNWTYVSAVHTEGN---YGESGMDAFKELAAQEGLCIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPDGQSLPPGRTKKPIAGVIGPGSSSVAIQVQNLLQLFDIPQIAYSATSIDLSDKTLYKY 200
VHVGTWHEGVLNIDDYKIQMNKSGVVRSVCSEPCLKGQIKVIRKG
                                   SMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEP-----DMIRDG 448
                                                                        SGEEVWFDEKGD---APGR----YDI-----MNLQYTE--
                                                                                                                                                  SGTF----GGILHEP----
                                                                                                                                                                                                                                                                                                    SDGWADRDEVIEGYE-VEANGGITIKLQSPEV---RSFDDYFLKLRLDTNTRNPWFPEFW 372
                                                                                                           HGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVV 409
                                                                                                                                                                                     P---GIYDEVVPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSI 349
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Pred. No.
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                                                                          ANRYDY 494
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Search completed: February 17, 2005, 16:08:02 Job time : 0.001 secs

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RESULT 1
AARO9301
ID AARO
XX AARO
AC AARO
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DT 27-F
DT 30-F
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Perfect score:
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                       24-OCT-2003
27-AUG-2003
25-MAR-2003
                                             03-MAY-1989;
                                                                         03-MAY-1989;
                                                                                                         15-NOV-1990.
                                                                                                                                     WO9013630-A.
                                                                                                                                                                Human immunodeficiency virus 1; isolate NDK
                                                                                                                                                                                              Human immunodeficiency virus; AIDS
                                                                                                                                                                                                                           Sequence deduced from pol gene of HIV 1-NDK
                                                                                                                                                                                                                                                                                                                                   AAR09301;
                                                                                                                                                                                                                                                                                                                                                               AAR09301 standard; protein;
              (INRM ) INSERM INST NAT SANTE & RECH MED
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length: 2000000000
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Match Length DB
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2623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aar09301.geneseqp1990s:*
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                                                                           89FR-00005914
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Search completed: February 17, 2005, 16:11:02 Job time : 0.001 secs

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Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            The HIV NDK virus was isolated from peripheral blood lymphocytes of an AIDS patient. A genomic library was prepd. from DNA extracted from CEM cells infected with the virus. The library was screened with a pBT1 probe corresp. to a fragment from HIV 1. The virus is more cytopathic than other strains and is not inhibited by OKT4A. It has been deposited as CNCM I-857. The sequence can be used to express proteins useful for diagnosing the presence of NDK and related viruses and in vaccines against immunodeficiency diseases. See also AAR09301-5. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA Field.) (Updated on 25-MAR-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                 Sequence 982 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New HIV-NDK retrovirus and protein component - used immuno-deficiency disorders and in raising MAbs for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1990-361470/48.
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 560
                                                                                                         402 NSSNKWVVSM----TLGLHPWIAN-IDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKM 456
                                                                                                                                               475 -----IYQEPFKNIKT------GKYARTRGAHTNDVKQLTEAVQKIATESI--VIWGK 519
                                                                                                                                                                                349 IHGIEGAFDEP--GTKTVIPGRVIGKFSIRLVPHMN-----VSAVEKQVTRHLEDVFSKR 401
                                                                                                                                                                                                                                                        298 EVVPLTEEEINTYKAIHLDLEEYRN--SSRVEKFLFDTKEEILMHL-----WRYPSLS 348
                                                                                                                                                                                                                      EVVPLTEE----AELELAENREILKEPVHGVYYDPSKDLIAELQKQGDGQWTYQ---
WYQLEKEPII----GAETFYVDGAANRETKLGKAGYV
                                   FQEIVHKSVVLIPLGAVD---DGEHSQNEKINRWNYI 490
                                                                       TPKFKLPIQKETWETWWIEYWQATWIPEWEFV----
                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                           Score 63.5;
Pred. No. 0;
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Result
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Search completed: February 17, 2005, 16:17:31 Job time : 0.001 secs
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                            Query Match 1.5%; Score 38.5; DB 1; Length 101; Best Local Similarity 25.3%; Pred. No. 0; Matches 19; Conservative 10; Mismatches 25; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Score Match Length DB ID
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                                                                                                                                                            242 GTRGNSYFMVEVKCR 256
                                                                                57 GSSGTTYYASWAKGR 71
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2623
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aar91823.genpept:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Result
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                        Cortactin; SH3 domain; binding peptide; Src homology region 3; tyrosine kinase; immune response; lymphokine; interleukin 1; Nck; Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
                                                                                       14-FEB-1997;
                                                                                                                     21-AUG-1997.
                                                                                                                                                    WO9730074-A1.
                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                      Peptide resembling an SH3 domain binding peptide SEQ ID NO:428.
                                                                                                                                                                                                                                                                                                      27-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                      AAW39029;
                                                                                                                                                                                                                                                                                                                                                                   AAW39029 standard; peptide; 15
           (CYTO-) CYTOGEN CORP.
(UYNC-) UNIV NORTH CAROLINA
                                                         16-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Search completed: February 17, 2005, 16:19:15
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Query Match
Best Local Similarity
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                                                                                                                                                                                                      The present sequence represents a peptide which resembles a Src homology cregion 3 (SH3) binding peptide. SH3 binding peptides are selected from: (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of Src; (e) peptides which bind the SH3 domain of Src; (e) peptides which bind the SH3 domain of Sh3 binding peptides which bind the sH3 domain of SH3 domain of Sh3 binding to Chair respective SH3 domains, which could be used to modulate the pharmacological activity of proteins or polypeptide containing the SH3 domain. The peptides can also be used to activate Src or Src-related CC protein tyrosine kinases, to stimulate the immune response by increasing CC the production of certain lymphokines, e.g. tumour necrosis factor-alpha CC and interleukin-1, or to deliver a conjugated molecule to certain CC cellular compartments containing Src or Src related proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sparks AB,
Rider JE;
                                                                                                                                                                        Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Src homology region 3 binding peptide - used to activate Src tyrosine kinase(s) and to stimulate immune response by increasing production of certain lymphokine(s), e.g. interleukin-1.
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                                      26 SSPSPPP 32
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Pred. No.
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BB ;
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us-09-731-872-242
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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241
                    240 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 299
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                                                                                                FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 239
TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV
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Copyright (c) 1993 - 2005 Compugen Ltd.
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	300 VPLTEE 301 VPLTEE 301 VPLTEE 360 GTKTVI 361 GTKTVI 420 ANIDDT	300 VPLTEBEINTYKAIHLDLEEYRNSSRVEKFLFDTKEBILMHLWRYPSLSIHGIBGAFDEP 359	
라 상	360 GTKTVI 361 GTKTVI	PGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNGSNKMVVSMTLGLHPWI 419 	
δ	420 ANIDDT	QYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 479	
망	421 ANIDDT	QYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480	
γQ	480 QNEKIN	480 QNEKINRWNYIEGTKLFAAFFLEMAQLH 507	
ф	481 QNEKIN	481 QNEKINEWNYIEGTKLFAAFFLEMAQLH 508	
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us-09-948-783-139
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Best Local Similarity 99.8
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                                                                     180 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 239
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                   240 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 299
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Copyright (c) 1993 - 2005 Compugen Ltd.
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htive 0; Mismatches
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	480 QNEKINRWNYIEGTKLFAAFFLEMAQLH 507	480	\$
48	421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 48	421	밁
47	420 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 47	420	Ş
42	361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 42	361	뮹
41	360 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 41	360	Ş
36	301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 36	301	뮹
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Best Local Similarity 99.8%;
Matches 507; Conservative
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                 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 299
                                                                                  FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 239
                                                                                                                                                                                                                                                                    MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI
TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDBV
                                                                 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match Length DB
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2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 seqs, 509 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.6
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               509 1 us-09-892-877-137
                                                                                                                                                                                                                                                                                                                                    Score 2612.5;
Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 509;
                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                     Indels 1; Gaps
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                                                                 240
300
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	481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508	481	ğ
	480 QNEKINRWNYIEGTKLFAAFFLEMAQLH 507	480	¥
480	421 ANIDDTQYLAAKRAIRTVFGTEPDMIKDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480	421	ઠ
479	420 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 479	420	¥
420	361 GTKTVIPGRVIGKFSIRLVPHMVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420	361	ŏ
419	360 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 419	360	₹
360	301 VPLTEBEINTYKAIHLDLEBYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360	301	b
359	300 VPLTESEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 359	300	₹

Search completed: February 17, 2005, 17:33:32 Job time: 0.001 secs

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Title:
Perfect score:
Sequence:
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No.
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Maximum DB
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us-09-791-389-2
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                          Query Match 97.8%; Score 2566.5; DB 1; Length 501; Best Local Similarity 99.4%; Pred. No. 0; Matches 498; Conservative 1; Mismatches 1; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2566.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
   241
                  247 SYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEE 306
                                                                       181
                                                                                                                                                                127 VCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD 186
                                                                                          187 LPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGN 246
                                                                                                                                           121 VCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                 61 VPRFRQELFXMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGT 120
                                                                                                                                                                                                                                    67 VPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGT 126
                                                                                                                                                                                                                                                                                      SYFMVEVKCRDODFHSGTFGGTLHEPMADLVALLGSLVDSSGHTLVPGTYDEVVPLTEEE
                                                                       LPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGN
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Match Length DB
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2623
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDPKLGRMAASLLAVLLLLL.....NYIEGTKLFAAFFLEMAQLH 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               February 17, 2005, 17:34:38; Search time 0.001 Seconds (without alignments) 254.007 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  us-09-791-389-2:*
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Copyright (c) 1993 - 2005 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                              1; Indels 1;
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                                                                       240
 300
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	bearch completed: February 17, 2005, 17:34:39	search completed:	4 03
	481 WNYIEGTKIFAAFFLEMAQIH 501)b 48	
	487 WNYIEGTKLFAAFFLEMAQLH 507)y 48	\sim
480	421 YLAAKKAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINR 480	უხ 42	•
486	427 YLAAKRAIRTVFGTEPDMIRDGSTIPIAKWFQEIVHKSVVLIPLGAVDDGEHSQNEKINR 486)y 42	\sim
420	361 GRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQ 420	ეხ 36	•
426	367 GRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKVVVSMTLGLHPWIANIDDTQ 426)у 36	\sim
360	301 INTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIP 360	ახ 30	
366	307 INTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIF 366	λλ 30	~

dob cime

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - protein search, using sw model
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                                        Score
    607.5
                                    Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   us-10-036-342-57
2623
1 MDPKLGRMAASILAVLLLLL......NYIEGTKLFAAFFLEMAQLH 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 segs, 148 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  February 17, 2005, 17:08:51; Search time 0.001 Seconds (without alignments) 75.036 Million cell updates/sec
    23.2
                                                                                                                                                                                                                          us-09-621-976-3957:*
148 1 us-09-621-976-3957
                                        Ħ
                                                                                                     SUMMARIES
                                    Description
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ALIGNMENTS

멍 Ś RESULT 1 us-09-621-976-3957 Query Match 23.2%; Best Local Similarity 96.9%; Matches 124; Conservative 60 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 119 Score 607.5; DB 1; Length 148; Pred. No. 0; O; Mismatches 3; Indels 1; 3; Indels 1;

Gaps

δ 밁 121 SDPTXXTV 128 120 SDPTKGTV 127

밁

61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELX 120

Search completed: February 17, 2005, 17:08:51 Job time : 0.001 secs

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Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB1108
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.;
Bloecker, H.; Brandt, P.; Chakraborty, T.; Charbit, A.; Chetouani, F.; Couve,
E.; de Daruvar, A.; Dehoux, P.; Domann, E.; Dominguez-Bernal, G.; Duchaud, E.;
Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Garcia-Del Portillo, F.;
Garrido, P.; Gautier, L.; Goebel, W.; Gomez-Lopez, N.; Hain, T.; Hauf, J.;
Jackson, D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.;
Maltaurnam, A.; Mata Vicente, J.; Ng, E.; Nordsiek, G.; Novella, S.; de Pablos,
B.; Perez-Diaz, J.C.; Remmel, B.; Rose, M.; Rusniok, C.; Schlueter, T.; Simoes,
N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, J.; Cossart, P.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
No.
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Roslecule type: DNA
A;Roslecule type: DNA
A;Cross-references: UNIPROT:Q9ZEY0; GB:NC_003210; PIDN:CAD00792.1;
PID:g16409630; GSPDB:GN00177
PID:g16409630; GSPDB:GN00177
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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    succinyldiaminopimelate desuccinylase homolog lmo0265 [imported]

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length:
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Match Length DB
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2623
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192.153 Million cell updates/sec
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Compugen Ltd.
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C;Genetics:
A;Gene: lmo0265
C;Superfamily: succinyl-diaminopimelate desuccinylase
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Best Local Similarity 23.0%;
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331
                                                                    272
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                                                                                                                                                                                                                                                                                                                   222 DYIVISDNLWISQRKPA---ITYGTRGNSYFMVEVKCRDQDFHSG--TFGGILHEPMADL
                                                                                                                                                                                                                                                                                                                                                          100
                                                                                                                                                                                                                                                                                                                                                                                       162 GATDNKGPVLAWINAVSAFRALEODLPVNIKFIIEGMBEAGSVALEELVEKEKDRFFSGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 LPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGR 161
                                                                                                                                                                                                                                                                                                                                                                                                                              49 -- DRASL-----VSEIGSSNEK-VLAFSGHMDVVDAGDVSKWKFPPFEATEHEGKLYGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 LHQDEFVQTLKEWVAIESDS--VQPVPRFRQELFRWMAVAADTLQRLGARVASVDMGPQQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \vdash
                                                                  INKLNKQENVNLELI-FDYDKQPVFSDKNSDLVHIAKSVASDIVKEEIPLLGISGTTDAA
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EFTK--AKKEFPVIIFGPGNETPHQVNENVSIGNYLE
                                 KMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIE 491
                                                                                                                                       NEILGDF-----IHNVT-VIDGGNQVNSIPEKAQLQGNIRSIPEMDNETV-KQVLVKI
                                                                                                                                                                          EEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHL
                                                                                                                                                                                                                                              VALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSRVEKFL--FDTK 334
                                                                                                                                                                                                                                                                                                                                                        GATDMKSGLAAMVIAMIELHEEKOKLNGKIRLLATVGEEIGELGAEOLTOK---GYADDL
                                                                                                   EDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIA 454
                                                                                                                                                                                                               -----VNAIDNLLL--FYNE----
                                                                                                                                                                                                                                                                                   DGLIIGE-----PSGHRIVYAHKGSINY--TVKSTGKNAHSSMPEFG-----
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Pred. No. 0;
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365
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Search completed: February 17, 2005, 16:21:08 Job time: 0.001 secs

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C;Accession: S56299; S62255; S53/71
R;Murakami, Y; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.;
S.I.; Sasanuma, M.; Tsuchiya, Y.; Soeda, E.; Yokoyama, K.; Yamaz
Tashiro, H.; Eki, T.
Tashiro, H.; Eki, T.
Submitted to the EMBL Data Library, May 1995
A:Description: Analysis of the nucleotide sequence of chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein YFR044c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein F006
C;Species: Saccharomyces cerevisiae
C;Date: 02-Sep-1995 #sequence revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: S56299; S62255; S63791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
No.
                                                                                                                              A;Moclecule type; DNA
A;Residues: 1-481 <MUR>
A;Residues: 1-61 <MUR>
A;Cross-references: UNIPROT:P43616; EMBL:D50617; NID:g836685; PIDN:BAA09283.1;
A;Cross-references: UNIPROT:P43616; EMBL:D50617; NID:g836685; PIDN:BAA09283.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                          A; Molecule type: DNA
A; Residues: 1-481 < MUW>
                                                                                submitted to the EMBL Data A;Reference number: S62230 A;Accession: S62255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
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Maximum Match 100%
Listing first 45 s
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                                                                                                                                                                                                                                                         A;Accession: S56299
Cross-references: EMBL:D44597; NID:g871938; PIDN:BAA08010.1; PID:d1008600;
VID:g871943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:D44597; NID:g871938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-481 < EKI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Eki, T.; Naitou, M.; Hagiwara, H.; Ozawa, M.; Sasanuma, Tsuchiya, Y.; Shibatta, T.; Hanaoka, F.; Murakami, Y. Yeast 12, 149-167, 1996
A;Title: Analysis of a 36.2 kb DNA sequence including the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position:
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Best Local Similarity 45.2%;
Matches 212; Conservative 8
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423
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                                                                                                                                                                     FDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMVVSAVEKQV
                                                                                                                                                                                                                                                                                                                          EKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILH
                                                                       QKHCDAKFKSLNSPNKCRTELIHDGAYWVSDPFNAQFTAAKKATKLVYGVDPDFTREGGS
                                                                                                                                                                                                                  EPMIDLMQVLGSLVDSKGKILIDGIDEMVAPLTEKEKALYKDIEFSVEELNAATGSKTSL
                                                                                                                                                                                                                                                    EPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSRVEKFL
                                                                                                                                                                                                                                                                                          KKEANGYFKGVDAVCISDNYWLGTKKPVLTYGLRGCNYYQTIIEGPSADLHSGIFGGVVA
                                                                                                                                                                                                                                                                                                                                                                  IDEAKGIMKGRGVTDDTGPLLSWINVVDAFKASGQEFPVNLVTCFEGMEESGSLKLDELI
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I PITLTFODALNTSVLLLPMGRGDDGAHSINEKLDISNFVGGMKTMAAY
                              IPIAKMFQEIVHKSVVLIPLGAVDDGEHSONEKINRWNYIEGTKLFAAF
                                                                                                       TRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGST
                                                                                                                                           YDKKEDILMHRWRYPSLSIHGVEGAFSAQGAKTVIPAKVFGKFSIRTVPDMDSEKLTSLV
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Pred. No. 0;
3; Mismatches 168;
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Search completed: February 17, 2005, 16:26:43 Job time: 0.001 secs

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C;Accession: S43745
R;Lopez, M.; Nicaud, J.; Vergnolle, C.; Kader, J.; Bankaitis, V.; Gaillardin, submitted to the EMBL Data Library, July 1993
A;Description: A phospholipid transfer protein is required for dimorphic transition in the yeast Yarrowia lipolytica.
A;Reference number: S43745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
No.
                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-497 <LOP>
A;Cross-references: UNIPROT:P45816; EMBL:L20972; NID:g311166; PID:g311167
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                                                                                                                                                                                                                                                                                                                                                         A; Accession: S43745
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - phosphatidylinositol-phosphatidylcholine transfer protein SEC14 - yeast (Yarrowia lipolytica)
;Species: Yarrowia lipolytica, Candida lipolytica
;Date: 03-May-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                          ;Genetics:
                                                                                                                                                                      ;Introne: 6/3; 9/2
;58-265/Domain: cellular retinaldehyde-binding protein homology
                                                                                                                                                                                                                                  ;Gene: SEC14
                                                                         Query Match 1.8%; Score 47; DB 1; Length 497; Best Local Similarity 28.2%; Pred. No. 0; Matches 40; Conservative 14; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
12 LLAVLLLLLERGMESSPSPPPALL-EKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRF 70
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MEDILINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.

Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,

Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,

Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,

Godowet B., Godowet B., Wann J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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ORFNames=UNQ1915;
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Genome Res. 13:2265-2270 (2003).

EMBL; AV358756; AAQ89116.1; -.

GO; GO:0008237; F:metallopeptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR002933; Peptidase M20.

Pfam; PF01546; Peptidase M20; T.

SEQUENCE 507 AA; 56692 MW; F3B51A9123C927C0 CRC64;
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MEDLINE=22388257; PubMed=12477992; DOI=10.1075/pnas
                                                                                                                                                                                                                                                        Chen J.M., Barrett A.J.;

"Cloning and sequencing of a second human homologue carboxypeptidase in peptidase family M20.";

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databa
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Glutamate carboxypeptidase-like protein 2 pre
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Best Local S
Matches 504
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CONFLICT
SEQUENCE
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InterPro; IPR002933; Peptidase M20.
InterPro; IPR002933; Peptidase M20.
IPR0017546; Peptidase M20; I
PROSITE; PS00758; ARGE DAPS CPG2 2; FALSE NEG.
PROSITE; PS00759; ARGE DAPS CPG2 2; FALSE NEG.
Carboxypeptidase; Hydrolase; Metalloprotease; Signal.
SIGNAL 1
27
Potential
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EMBL; BC004271; -; NOT_ANNO:
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                    VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP
                                                                                                TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV
                                                                                                                                                     PRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKLAI
                                                                                                                                                                           FRALEQDLFVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKFAI
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                                                                            TYGTRGNSYFMVEVKCRDQDFHSGTFGG1LHELMADLVALLGSLVDSSGH1LVPG1YDEV
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L -> P (in Ref. 2).
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Pred. No. 0;
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Search completed: February 17, 2005, 16:38:39 Job time : 0.001 secs	481 QNEXINKWNYIEGTKLFAAFFLEWAQLH 508	QNEKINRWNYIEGTKLFAAFFLEMAQLH 507	421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480	420 ANIDDTQYLAAKRAIRTVFGTEFDMIRDGSTIFIAKMFQEIVHKSVVLIFLGAVDDGEHS 479	361 GTKTVIPGRVIGKFSIRLVPHMVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420	360 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 419

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RESULT 1
Q6ZND4
ID Q6ZN
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Perfect score:
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                                  TISSUE=Thalamus;
Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T.,
Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kiuchi H., Kanda K.,
Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
Masuho Y., Nagai K., Isogai T.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein FLJ16195.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6ZND4;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ16195.
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        171 AA;
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Copyright (c) 1993 - 2005 Compugen Ltd.
18880 MW; 20816D6D8F214688 CRC64;
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Query Match

29.2%; Score 766; DB 1; Length 171;

Job time : 0.001 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Result No. Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Title: Perfect score: Database : Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Total number of hits satisfying chosen parameters: Searched: Run on: OM protein - protein search, using sw model Scoring table: Sequence: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Query Score Match Length DB 766 BLOSUM62 Gapop 10.0 , Gapext 0.5 us-10-036-342-57 2623 1 seqs, 171 residues 1 MDPKLGRMAASLLAVLLLLL.....NYIEGTKLFAAFFLEMAQLH 507 February 17, 2005, 17:06:12; Search time 0.001 Seconds (without alignments) 86.697 Million cell updates/sec 29.2 bad18441.genpept:* 171 1 BAD18441 ij SUMMARIES Description

RESULT 1 BAD18441

ALIGNMENTS

Search completed: February 17, 2005, 17:06:12 Job time : 0.001 secs

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121 EIVHKSVVLIPLGAVDDGEHSQNEKINR 148